

pRL4

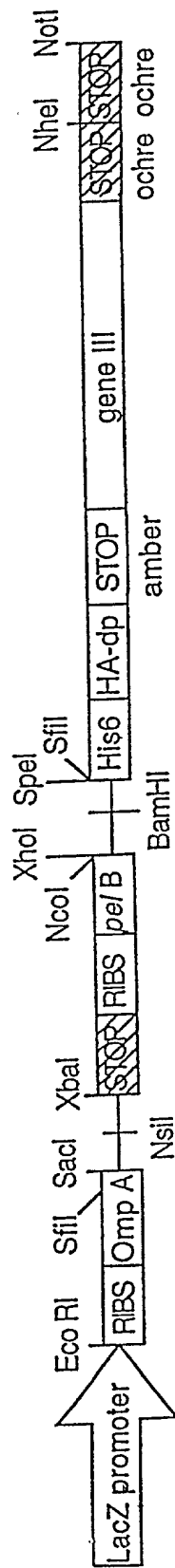


Fig. 1

Human Antibody sequence (TT sequence) (SEQ ID NO: 54)

Heavy Chain: cloning sites Xho I and Spe I are underlined

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1      11
gag gtg cag ctg CTC GAG CAG TCT GGG GCT GAG GTG AAG AAG CCT GGG TCC TCG GTG AAG
glu val gln leu leu glu gln ser gly ala glu val lys lys pro gly ser ser val lys
21      31
GTC TCC TGC AGG GCT TCT GGA GGC ACC TTC AAC AAT TAT GCC ATC AGC TGG GTG CGA CAG
val ser cys arg ala ser gly gly thr phe asn asn tyr ala ile ser trp val arg gln
41      51
GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA GGG ATC TTC CCT TTC CGT AAT ACA GCA AAG
ala pro gly gln gly leu glu trp met gly gly ile phe pro phe arg asn thr ala lys
61      71
TAC GCA CAA CAC TTC CAG GGC AGA GTC ACC ATT ACC GCG GAC GAA TCC ACG GGC ACA GCC
tyr ala gln his phe gln gly arg val thr ile thr ala asp glu ser thr gly thr ala
81      91
TAC ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC ACG GCC ATA TAT TAT TGT GCG AGA GGG
tyr met glu leu ser ser leu arg ser glu asp thr ala ile tyr tyr cys ala arg gly
101     111
GAT ACG ATT TTT GGA GTG ACC ATG GGA TAC TAC GCT ATG GAC GTC TGG GGC CAA GGG ACC
asp thr ile phe gly val thr met gly tyr tyr ala met asp val trp gly gln gly thr
121     131
ACG GTC ACC GTC TCC GCA GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC
thr val thr val ser ala ala ser thr lys gly pro ser val phe pro leu ala pro ser
141     151
TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC
ser lys ser thr ser gly gly thr ala ala leu gly cys leu val lys asp tyr phe pro
161     171
GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG
glu pro val thr val ser trp asn ser gly ala leu thr ser gly val his thr phe pro
181     191
GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC
ala val leu gln ser ser gly leu tyr ser leu ser ser val val thr val pro ser ser
201     211
AGC TTG GGC ACC CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG
ser leu gly thr gln thr tyr ile cys asn val asn his lys pro ser asn thr lys val
221     231
GAC AAG AAA GTT GAG CCC AAA TCT TGT GAC AAA act aqt
asp lys lys val glu pro lys ser cys asp lys thr ser

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Fig. 2A

Human Antibody Sequence (TT sequence) (SEQ ID NO: 55)

Light Chain: cloning sites Sac I and Xba I are underlined

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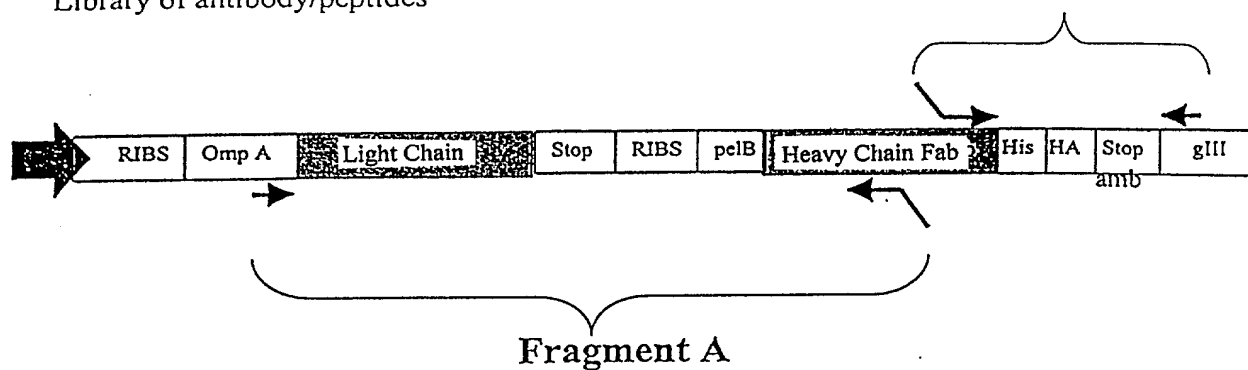
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glu leu thr gln ser pro gly thr leu ser leu ser pro gly glu arg ala thr leu ser
21          31
tgc agg gcc agt cac agt gtt agc agg gcc tac tta gcc tgg tac cag cag aaa cct ggc
cys arg ala ser his ser val ser arg ala tyr leu ala trp tyr gln gln lys pro gly
41          51
cag gct ccc agg ctc ctc atc tat ggt aca tcc agc agg gcc act ggc atc cca gac agg
gln ala pro arg leu leu ile tyr gly thr ser ser arg ala thr gly ile pro asp arg
61          71
ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag cct gaa
phe ser gly ser gly ser gly thr asp phe thr leu thr ile ser arg leu glu pro glu
81          91
gat ttt gca gtg tac tac tgt cag cag tat ggt ggc tca ccg tgg ttc ggc caa ggg acc
asp phe ala val tyr tyr cys gln gln tyr gly gly ser pro trp phe gly gln gly thr
101         111
AAG GTG GAA CTC AAA CGA ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT
lys val glu leu lys arg thr val ala ala pro ser val phe ile phe pro pro ser asp
121         131
GAG CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT CCC AGA
glu gln leu lys ser gly thr ala ser val val cys leu leu asn asn phe tyr pro arg
141         151
GAG GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT
glu ala lys val gln trp lys val asp asn ala leu gln ser gly asn ser gln glu ser
161         171
GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG CTG AGC
val thr glu gln asp ser lys asp ser thr tyr ser leu ser ser thr leu thr leu ser
181         191
AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC
lys ala asp tyr glu lys his lys val tyr ala cys glu val thr his gln gly leu ser
201         211
TTG CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG TGT TAG Ttc taq a
leu pro val thr lys ser phe asn arg gly glu cys AMB

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Fig. 2B

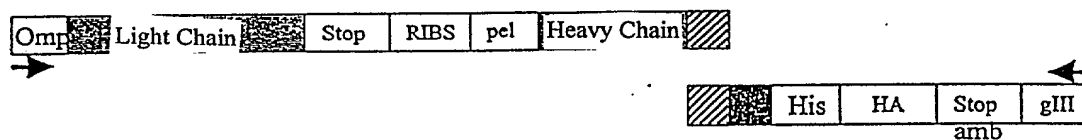
Library of antibody/peptides

Fragment B



Fragment A

Fragment B



HCDR3 Library



Fig. 4

SEQ. ID NO.

AMINO ACID SEQUENCE

CLONE

X1a	Pro-Pro-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Gly-Gly	25
	CCG-CCC-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-GGA-GGC	26
X1a-11	Gly-Gly-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Gly-Gly	27
	GGG-GGT-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-GGA-GGC	28
X1a-13	Gly-Gly-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Gly-Gly	29
	GGC-GGT-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-GGA-GGC	30
X1c	Trp-Leu-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Val	31
	TGG-CTG-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCT-GTC	32
X2c	Met-Ile-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Val-Gly	33
	ATG-ATA-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-GTT-GGC	34
X3a	Val-Val-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Val	35
	GTG-GTA-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCT-GTT	36
X3b	Gly-Pro-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Asp	37
	GGG-CCG-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCC-GAT	38
X4b	Leu-Pro-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Val	39
	TTG-CCA-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCT-GTT	40
X4c	Ser-Leu-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Ile	41
	TCA-CTG-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCC-ATC	42
X5a	Thr-Met-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Val	43
	ACA-ATG-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCC-GTT	44
X5c	Thr-Thr-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Val	45
	ACG-ACA-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCT-GTC	46
X7a	Thr-Arg-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Cys-Ser	47
	ACA-CGG-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-TGC-AGC	48
X7b	no peptide deletion mutant	
X7c	Gln-Thr-Ile-Glu-Gly-Pro-Thr- Leu-Arg-Gln-Trp- Leu-Ala-Ala-Arg- Ala-Pro-Asp	49
	CAG-ACA-ATT-GAA-GGG-CCG-ACG-CTG-CGG-CAA-TGG-CTG-GCG-GCG-GCG-CCT-CAC	50

Fig. 5

pRL8

(SEQ ID NO: 60)

GGGAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTGTAA
ATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGC AAAATCCCTTATAAATC
AAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAACAAGAGT
CCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATC
AGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTC
GAGGTGCCGTAAAGCACTAAATCGGAACCTAAAGGGAGCCCCCGATTAGA
GCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGC
GAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGT
AACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGC
ACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACA
TTCAAATATGTATCCGCTCATGAGACAATAACCCGTGATAAATGCTTCAATAAT
ATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCC
TTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAA
GTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAACTGG
ATCTCAACAGCGGTAAGATCCTTGAGAGTTTTTCGCCCCGAAGAACGTTTTCCA
ATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGA
CGCCGGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAATGACTTG
GTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAA
GAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTT
ACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAAC
ATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAG
CCATACCAAACGACGAGCTGTACACCACGATGCCTGTAGCAATGGCAACAAC
GTTGCGCAAACATTAACCTGGCGAACTACTTACTCTAGCTTCCCGGCAACAAT
TAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGC
CCTTCGGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGT
CTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGT
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GATCGCTGAGATAGGTGCCTCACTGATTAAGCATTTGGTAACCTGTCAGACCAA
GTTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTTAATTTAAAGG
ATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGA
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GAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACCACCG
CTACCAGCGGTGGTTTGTGTCGGATCAAGAGCTACCAACTCTTTTTCCGAA
GGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAG
CCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGC
TCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTA
CCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGGCGCAGCGGTCCGGGCTG
AACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGA

Fig. 6A

ACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGG
AGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGC
ACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGT
TTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGG
AGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTG
CTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAA
CCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACC
GAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAA
CCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCAGGACAGGTT
TCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTC
ACTCATTAGGCACCCACAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTG
TGGAATTGTGAGCGGATAACAATTGAATTCAGGAGGAATTTAAAATGAAAAA
GACAGCTATCGCGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTGGCCCAAG
GCGGCCGAGCTCGGCCATGGCTGGTTGGGCAGCGAGTAATAACAATCCAGCG
GCTGCCGTAGGCAATAGGTATTTTATTATGACTGTCTCCTTGGCGACTAGCTA
GTTTAGAATTCGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTGTTATCC
GCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCTGG
GGTGCCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCG
TTCCAGTCGGGAAACCTGTGCTGTTACTAATGATGGTGATGGTGATGGCTAG
TTTTGTGACAAGATTTGGGCTCAACTTCTGTGTCACCTTGGTGTTGCTGGGCT
TGTGATTCACGTTGCAGATGTAGGTCTGGGTGCCCAAGCTGCTGGAGGGCAC
GGTCACCACGCTGCTGAgGGAGTAGAGTCTGAGGACTGTAGGACAGCCGGG
AAGGTGTGCACGCCGCTGGTCAgGGCGCCTGAgTTCCACGACACcGTCGCCGG
TTCgGGGAAGTAGTCCTTGACCAGGCAGCCAGGGCCGCTGTGCCCCCAGAG
GTGCTCTTGGAGGAGGGTGCCAGGGGGAAGACCGATGGGCCCTTGGTGAG
GCTGCGGAGACGGTGACCGTGGTACCAGCAGAAACCTGGCCAGGCTCCCAG
GCTCCTCATCTATGGTACATCCAGCAGGGCCACTGGCATCCCAGACAGGTTT
AGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGC
CTGAAGATTTTGCAGTGTACTACTGTGAGCAGTATGGTGCTCACCCTGGTTC
GGCCAAGGGACCAAGGTGGAACCTCAAACGAACTGTGGCTGCACCATCTGTCT
TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTGTG
TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAG
CAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGA
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCacccatcagggcctgagltgccccgtcac
aaagagcttcaacggaggagagtgttaarTCTAGATAATTAATTAGGAGGAATTTAAAATGAA
ATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAG
CCATGGCCGAGGTGCAGCTGCTCGAGATGAGCGATAAAATTATTCACCTGAC
TGACGACAGTTTTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTC
GATTTCTGGGCAGAGTGGTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGG
ATGAAATCGCTGACGAATATCAGGGCAAACCTGACCGTTGCAAACTGAACAT
CGATCAAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTATCCCGACT
CTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAAAGTGGGTGCACTTG
TCTAAAGGTCAGTTGAAAGAGTTCCTCGACGCTAACCTGGCGTACCCGTACG
ACGTTCCGGACTACGGTTCTACTAGTccgaaaccgtctacccacccggctcttctcggtggccgc
atcgccccgtctggaggaaaaagtgaaaaccctgaaagctcagaactccgagctggcgtccactgccaacatgctgcgcgaac

Fig. 6B

aggtggcacagctgaacagaaagtatgaacatggcggltgtgctagtGGCCAGGCCGGCCAGCACCAT
CACCATCACCATGGCGCATACCCGTACGACGTTCCGGACTACGCTTCTTAGG
AGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGCTCTGAGGGAGG
CGGTTCCGGTGGTGGCTCTGGTTCGGTGATTTTGATTATGAAAAGATGGCAA
ACGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACGCGCTACAGTC
TGACGCTAAAGGCAAACCTTGATTCTGTCGCTACTGATTACGGTGCTGCTATCG
ATGGTTTCATTGGTGACGTTTCCGGCCTTGCTAATGGTAATGGTGCTACTGGT
GATTTTGCTGGCTCTAATTCCCAAATGGCTCAAGTCGGTGACGGTGATAATTC
ACCTTTAATGAATAATTTCCGTCAATATTTACCTTCCCTCCCTCAATCGGTTGA
ATGTCGCCCTTTTGTCTTTAGCGCTGGTAAACCATATGAATTTTCTATTGATTG
TGACAAAATAAACTTATTCCGTGGTGTCTTTGCGTTTCTTTTATATGTTGCCAC
CTTTATGTATGTATTTTCTACGTTTGCTAACATACTGCGTAATAAGGAGTCTTA
AGCTAGCTAATTAATTTAAGCGGCCGCAGATCT

Fig. 6C

pRL8



Fig. 7

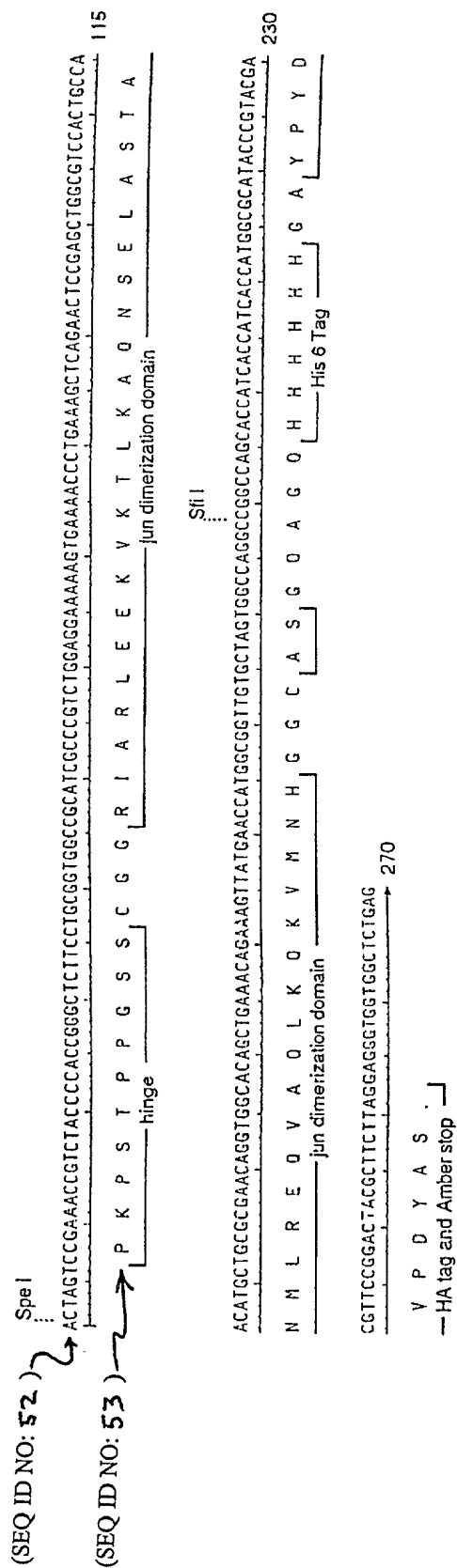


Fig. 8

TPO Positive Clones nnk nnk nnk nnk
 1 2 IEGPTLRQWLAARA 3 4

	Sample	nnk	nnk	nnk	nnk	Amino Acids		Amino Acids		
		1	2	3	4	1	2	3	4	
HC CDR3	X1c	tgg	ctg	cct	gtc	Trp	Leu	Pro	Val	
	X3a	gtg	gta	cct	gtt	Val	Val	Pro	Val	
	X3b	ggg	ccg	ccc	gat	Gly	Pro	Pro	Asp	
	X4b	ttg	cca	cct	gtt	Leu	Pro	Pro	Val	
	X4c	tca	ctg	ccc	atc	Ser	Leu	Pro	Ile	
	X5a	aca	atg	ccc	gtt	Thr	Met	Pro	Val	
	X5c	acg	aca	cct	gtc	Trp	Leu	Pro	Val	
	X7c	cag	aca	cct	cac	Gln	Thr	Pro	Asp	
HC CDR2	24	ctt	tat	tct	aat	Leu	Tyr	Ser	Asn	
	39	act	tac	ttg	cat	Thr	Tyr	Leu	His	
	3	agg	atg	ctc	gag	Arg	Met	Leu	Glu	
	7	aag	gaa	tct	aag	Lys	Glu	Ser	Lys	
	8	gcg	cat	gtg	cag	Ala	His	Val	Gln	
	10	cag	gag	att	agt	Gln	Glu	Ile	Ser	
	11	cgg	aat	aat	ccg	Arg	Asn	Asn	Pro	
	19	cag	cta	aat	tct	Gln	Leu	Asn	Ser	
	25	agt	att	ttt	gtc	Ser	Ile	Phe	Val	
	28	ggg	ccc	act	agt	Gly	Pro	Thr	Ser	
LC CDR1	10	aag	ggc	gtt	agt	Lys	Gly	Val	Ser	
	11	cat	ggg	gtg	gct	His	Gly	Val	Ala	
	12a	cgt	acg	atg	gct	Arg	Thr	Met	Ala	
	12b	cgt	ggc	gtt	aat	Arg	Gly	Val	Asn	
	14	cgt	tcg	ctt	gcg	Arg	Ser	Leu	Ala	
	16	cgg	ggc	gtt	gcg	Arg	Gly	Val	Ala	
	18	agg	acg	gtg	tct	Arg	Thr	Val	Ser	
	47	aag	ggg	gtg	gcg	Lys	Gly	Val	Ala	
LC CDR2	1	aat	ccg	agg	ggc	Asn	Pro	Arg	Gly	
	2	tcg	cct	cgg	agt	Ser	Pro	Arg	Ser	
	3	tcg	cct	cgt	acg	Ser	Pro	Arg	Thr	
	4	tcg	cct	tgg	cgt	Ser	Pro	Trp	Arg	
	5	act	ccg	aat	tgg	Thr	Pro	Asn	Trp	
	6	aat	cct	gcg	agg	Asn	Pro	Ala	Arg	
	7	aat	ccg	tcg	ggg	Asn	Pro	Ser	Gly	
	9	aat	cct	tat	tag	Asn	Pro	Tyr	Stop	
	10	aat	ccg	cgg	tct	Asn	Pro	Arg	Ser	
	11	aat	ccg	gat	gtg	Asn	Pro	Asp	Val	
	12	tcg	ccg	tcg	cgg	Ser	Pro	Ser	Arg	
	13	aat	cct	ctg	ttt	Asn	Pro	Leu	Phe	
	14	aat	ctt	ggg	tat	Asn	Pro	Gly	Tyr	
	15	aat	cct	att	agt	Asn	Pro	Ile	Ser	
	16	aat	cct	cag	cgg	Asn	Pro	Gln	Arg	
	18	aat	ccg	cgg	acg	Asn	Pro	Arg	Thr	
	19	aat	ccg	cgt	ggg	Asn	Pro	Arg	Gly	
	20	cat	ttg	aga	ctg	His	Leu	Arg	Leu	
	21	aag	tag	att	tat	Lys	Stop	Ile	Tyr	
	23	aat	cct	ggc	aag	Asn	Pro	Gly	Lys	
	24	aat	cct	cgt	ggg	Asn	Pro	Arg	Gly	
	26	aat	cct	aat	gtg	Asn	Pro	Asn	Val	
	27	tct	ccg	cgg	gtt	Ser	Pro	Arg	Val	
	29	acg	cct	cgg	ggc	Thr	Pro	Arg	Gly	
		30	cct	tag	tgg	tgg	Pro	Stop	Trp	Trp

FIG. 9

Activity of Fab clones containing 2 TPO mimetic peptides

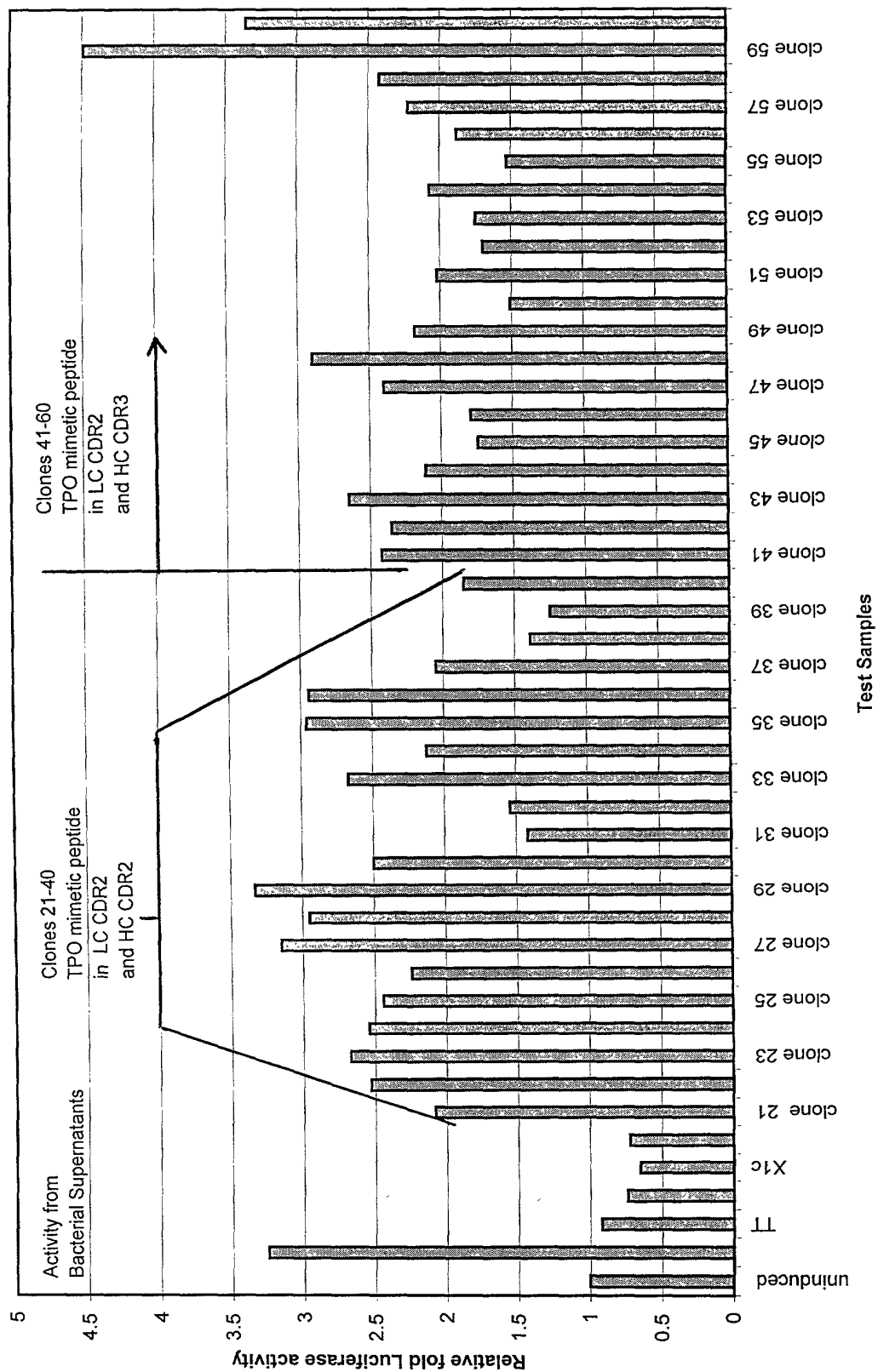


FIGURE 10

Activity of Fab clones containing 2 or 3 TPO mimetic peptides

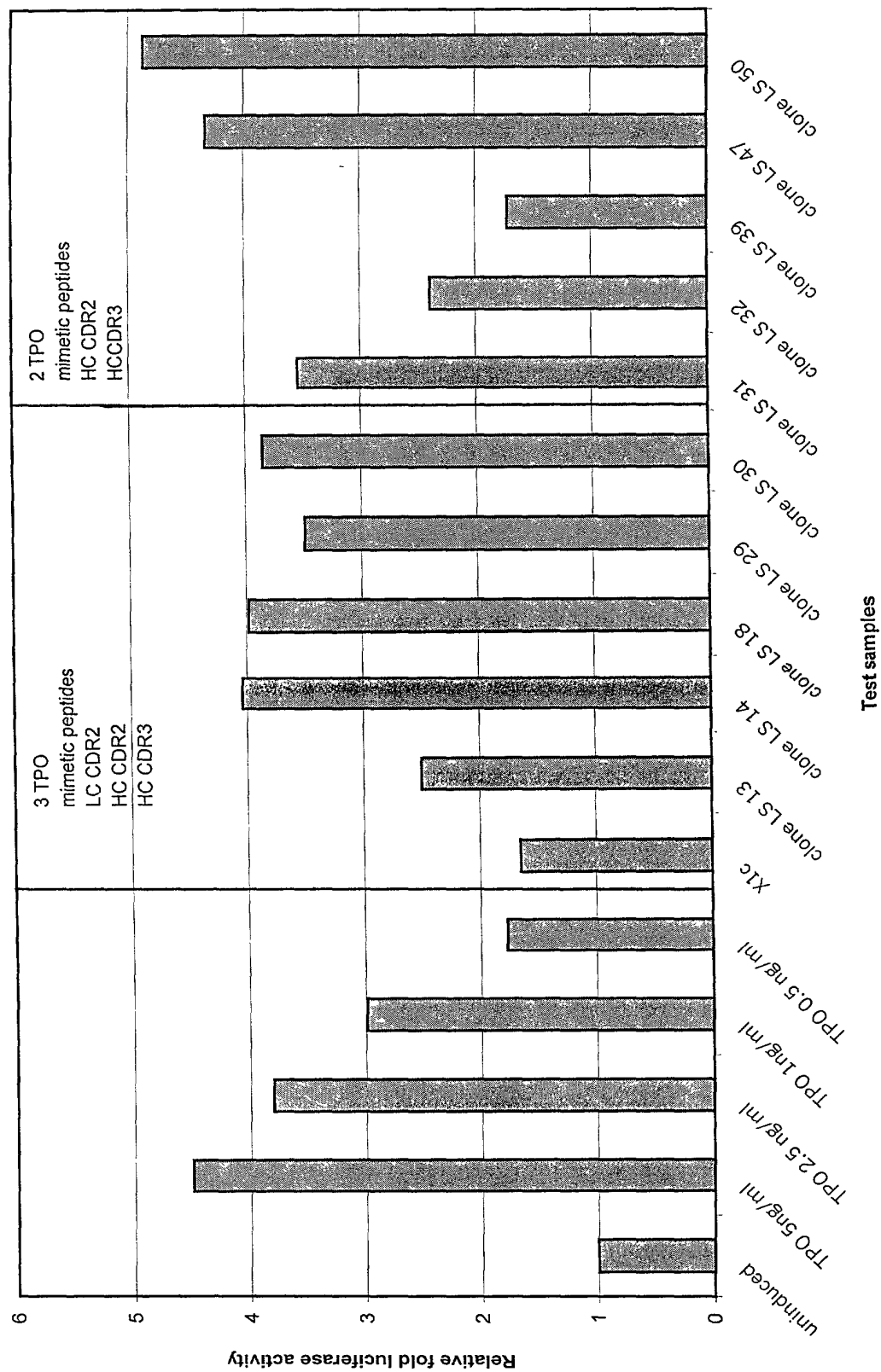


FIGURE 11

TPO Mimetic Activity of semi-purified Fab clone 59

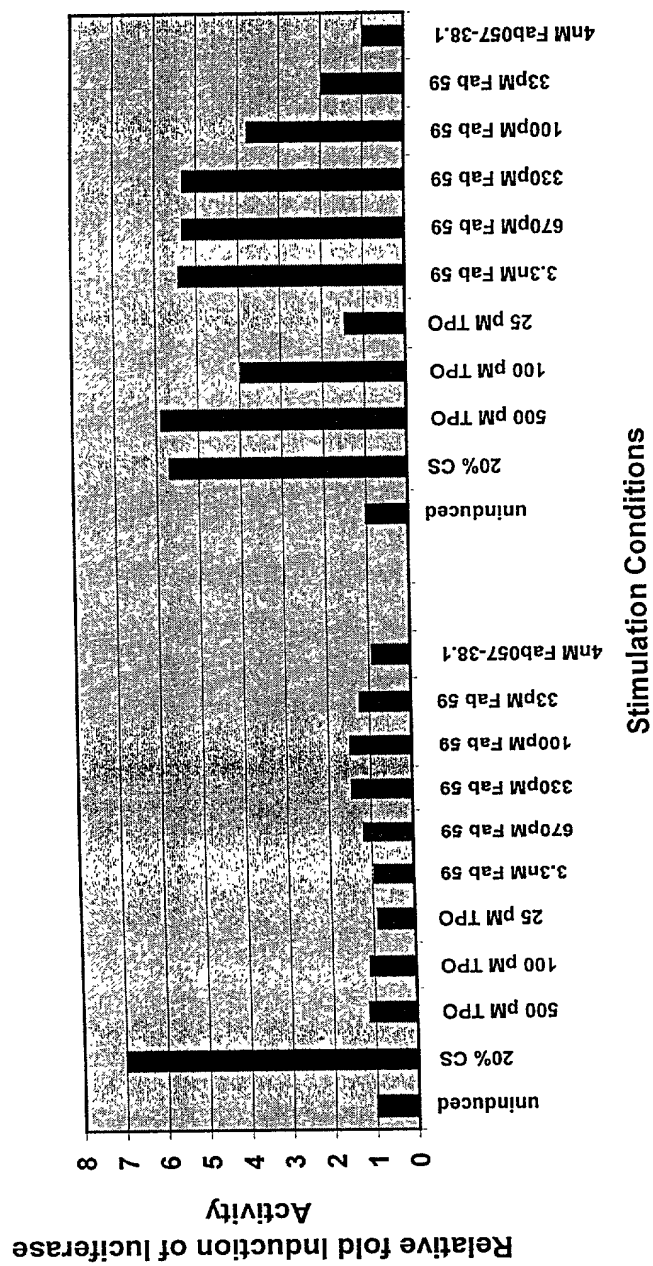


Fig. 12

(SEQ ID NO: 67)

5G1.1 – TPO Heavy Chain (Bold denotes TPO mimetic) Amino acid sequence:

MKWSWVILFLLSVTAGVHSQVQLVQSGAEVKKPGASVKVSCKASGYIFSNYWIQW
VRQAPGQGLEWMGEILPGSGSTEYTENFKDRVTMTRDTSTSTVYMESSLRSED
TAVYYCARLPIEGPTLRQWLAARAPVWGQGLTVTVSSASTKGPSVFPLAPCSR
STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV
PSSNFGTQTYTCNVDHKPSNTKVDKTVKCCVECPPCAPPVAGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQ
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRL
TVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK.

(SEQ ID NO: 68)

5G1.1 – TPO Heavy Chain (Bold denotes TPO mimetic) Nucleic acid sequence:

ATGAAGTGGAGCTGGGTTATTCTCTTCCTCCTGTCAGTAACTGCCGGCGTCCA
CTCCCAAGTCCAAGTGGTGAATCCGGCGCCGAGGTCAAGAAGCCAGGGGCC
TCAGTCAAAGTGTCTGTAAAGCTAGCGGCTATATTTTTCTAATTATTGGAT
TCAATGGGTGCGTCAGGCCCCCGGGCAGGGCCTGGAATGGATGGGTGAGATC
TTACCGGGCTCTGGTAGCACCGAATATACCGAAAATTTTAAAGACCGTGTTA
CTATGACGCGTGACACTTCGACTAGTACAGTATACATGGAGCTCTCCAGCCTG
CGATCGGAGGACACGGCCGTCTATTATTGCGCGCGTTTGCCAATTGAAGGG
CCGACGCTGCGGCAATGGCTGGCGGGCGCGCGCGCCTGTTTGGGGTCAAG
GAACCCTGGTCACTGTCTCGAGCGCCTCCACCAAGGGCCCATCCGTCTCCCC
CTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCC
TGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGC
CCTGACCAGCGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCT
ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGAC
CTACACCTGCAACGTAGATCACAAGCCAGCAACACCAAGGTGGACAAGAC
AGTTGAGCGCAAATGTTGTGTCGAGTGCCACCGTGCCAGCACCACCTGTG
GCAGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTACGTCGCTGGTGGTGGACGTGAGCCAGGAAGAC
CCCGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCA
AGACAAAGCCGCGGGAGGAGCAGTTCAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAA
GGTCTCCAACAAAGGCCTCCCGTCTCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAG
GAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTACC
CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC
ACAAGACCACGCTCCCGTGTGGTACTCCGACGGCTCCTTCTTCTCTACAGC
AGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCT
CCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCT
GTCTCTGGGTAAATGA

Fig. 13A

(SEQ ID NO: 69)

5G1.1 Light Chain Amino Acid Sequence

MDMRVPAQLLGLLLWLRGARCDIQMTQSPSSLSASVGDRVITITCGASENIYGALN
WYQQKPGKAPKLLIYGATNLADGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQ
NVLNTPITFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKSFNRGEC.

(SEQ ID NO: 70)

5G1.1 Light Chain Nucleic Acid Sequence

ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCG
AGGTGCCAGATGTGATATCCAGATGACCCAGTCCCGTCCCTGTCCGCCT
CTGTGGGCGATAGGGTCACCATCACCTGCGGCGCCAGCGAAAACATCTATGG
CGCGCTGAACTGGTATCAACAGAAACCCGGGAAAGCTCCGAAGCTTCTGATT
TACGGTGCGACGAACCTGGCAGATGGAGTCCCTTCTCGCTTCTCTGGATCCGG
CTCCGGAACGGATTTCACTCTGACCATCAGCAGTCTGCAGCCTGAAGACTTC
GCTACGTATTACTGTCAGAACGTTTTAAATACTCCGTTGACTTTCGGACAGGG
TACCAAGGTGGAAATAAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCC
CGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTG
AATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACA
GCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGA
AACACAAAGTCTACGCCTGCGAAGTACCCATCAGGGCCTGAGCTCGCCCGT
CACAAAGAGCTTCAACAGGGGAGAGTGTTAG

Note: Italics denotes leader sequence

Fig. 13B

FACS staining on transfected 293 cells

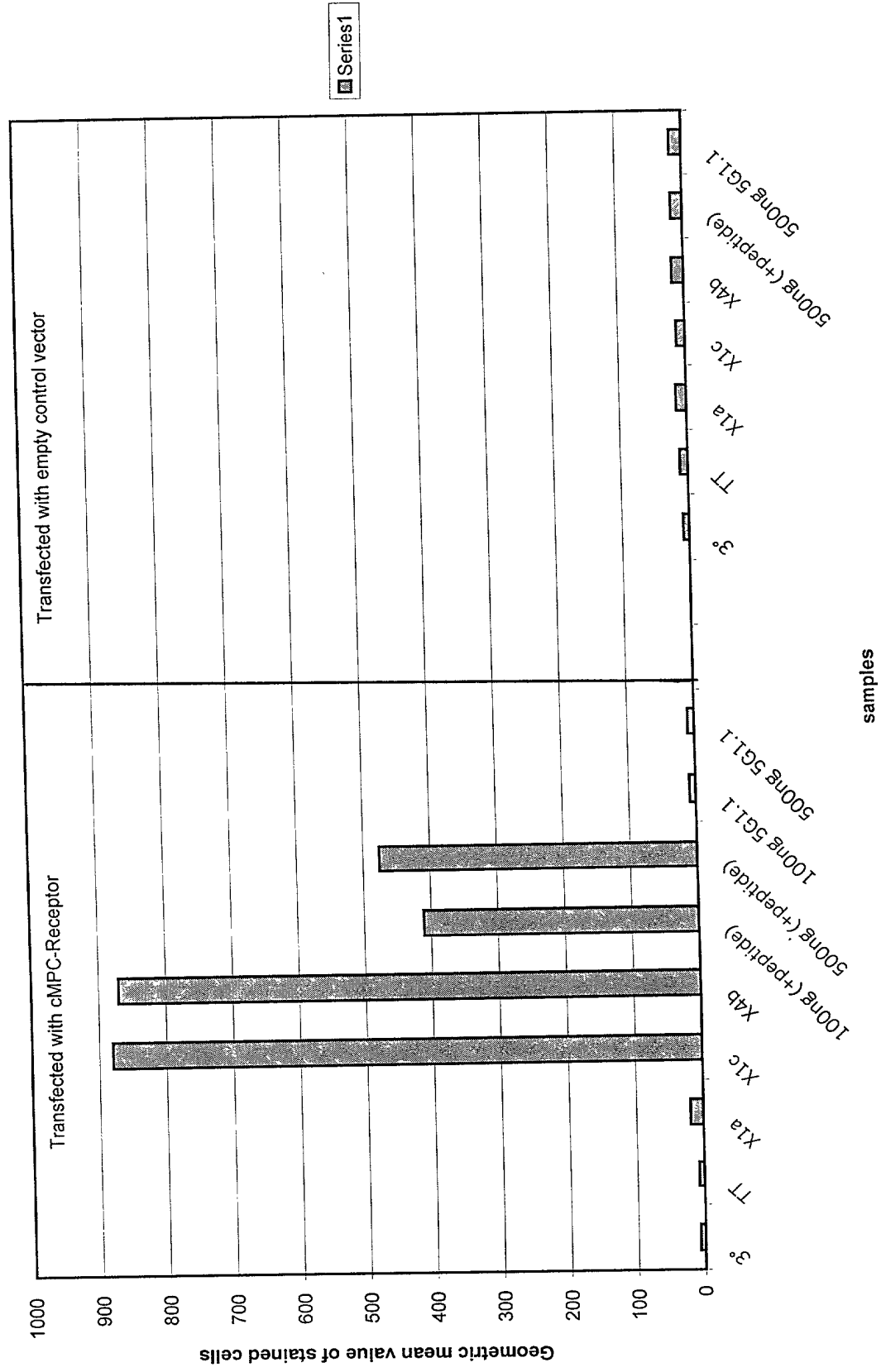


FIGURE 14

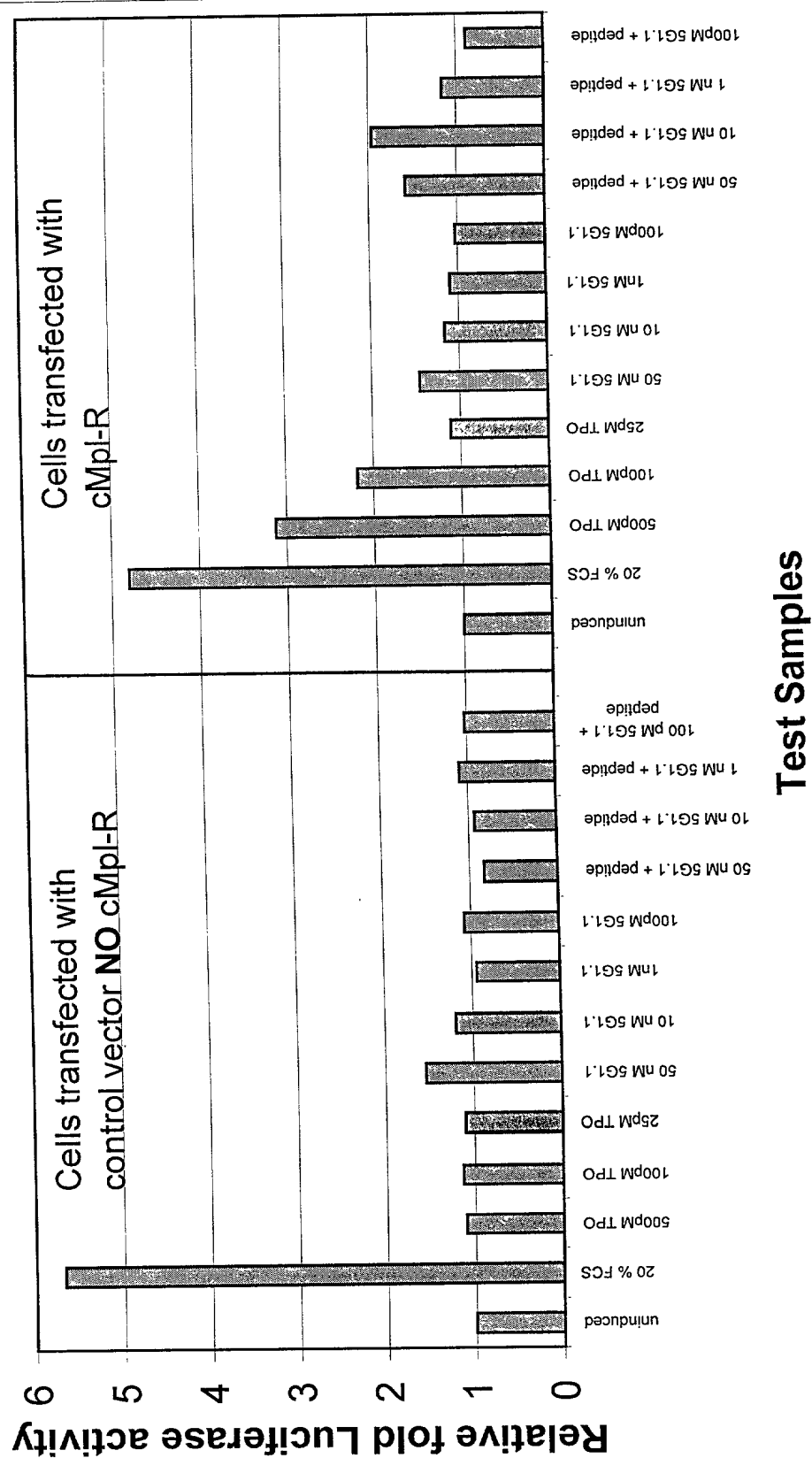


FIGURE 15

VARIABLE REGION OF 4-29 LIGHT CHAIN

(SEQ ID NO: 116)

1 GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGC CGG GCG AGT CAG ...
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
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 13
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 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 27a
 27b
 27c
 27d
 27e
 27f
 28
 ...AGT

Grafted CDR2

29 ATT AGT AGT TTG CTG GCC TGG TAT CAG CAG AAA CCA GGG AAA GCT CCT AAG CTC CTG ATC TAT AAC CCG ATC GAA GGC CCA ACC CTG CGC CAG TGG CTG GCT
 30
 31
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 52
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 52b
 52c
 52d
 52e
 52f
 52g
 52h
 52i
 52j

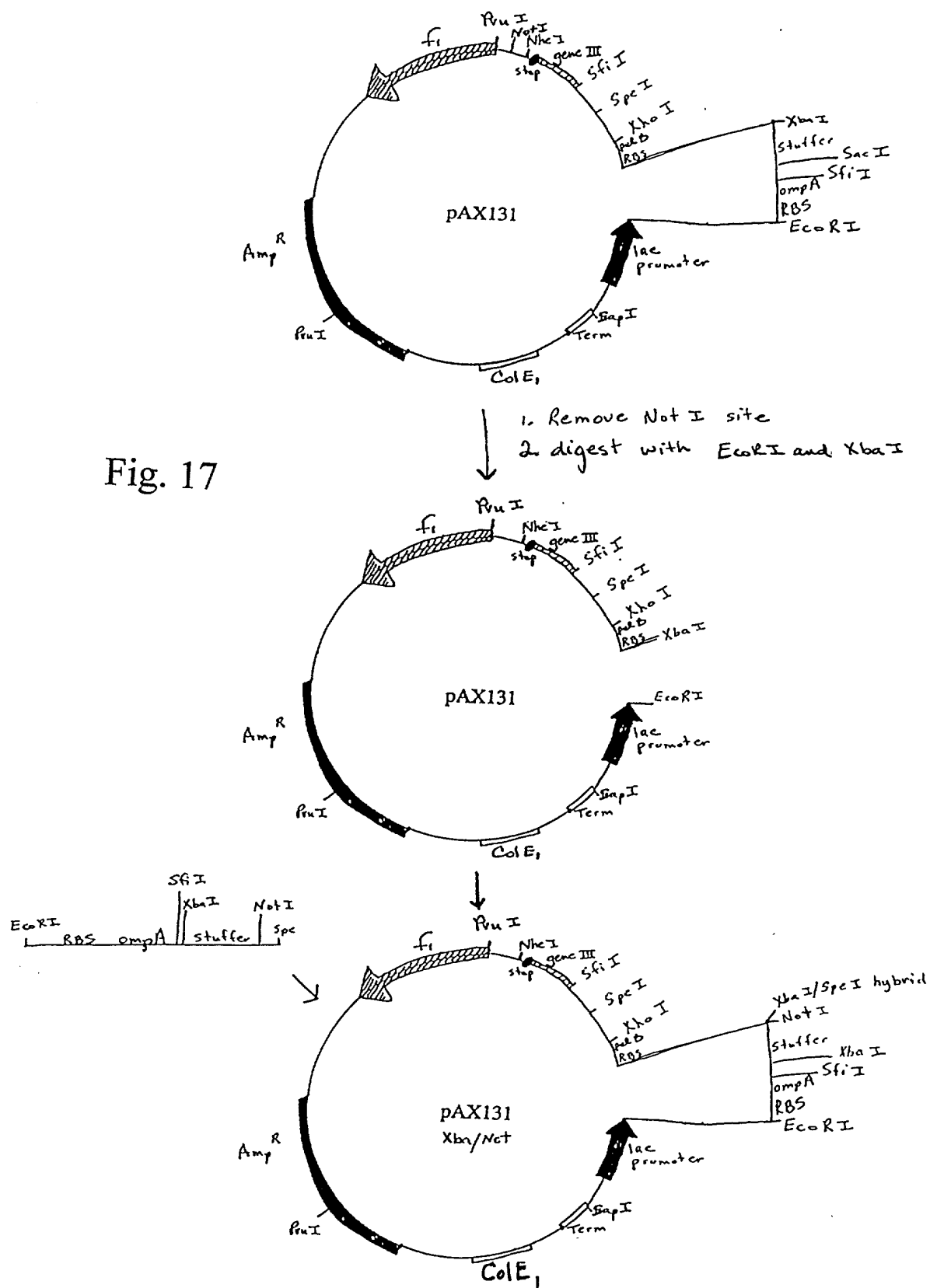
Grafted CDR2

52k ACT CGC GCT CGT GGT GGC GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT
 53
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 83
 84
 85

CDR3

86 TAT TAC TGC CAA CAG TAT AAT AGT TAC CCT CCC ACT TTC GGC CCT GGG ACC AAA GTG GAT ATC AAA
 87
 88
 89
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 93
 94
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 102
 103
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 105
 106
 107

Fig. 16



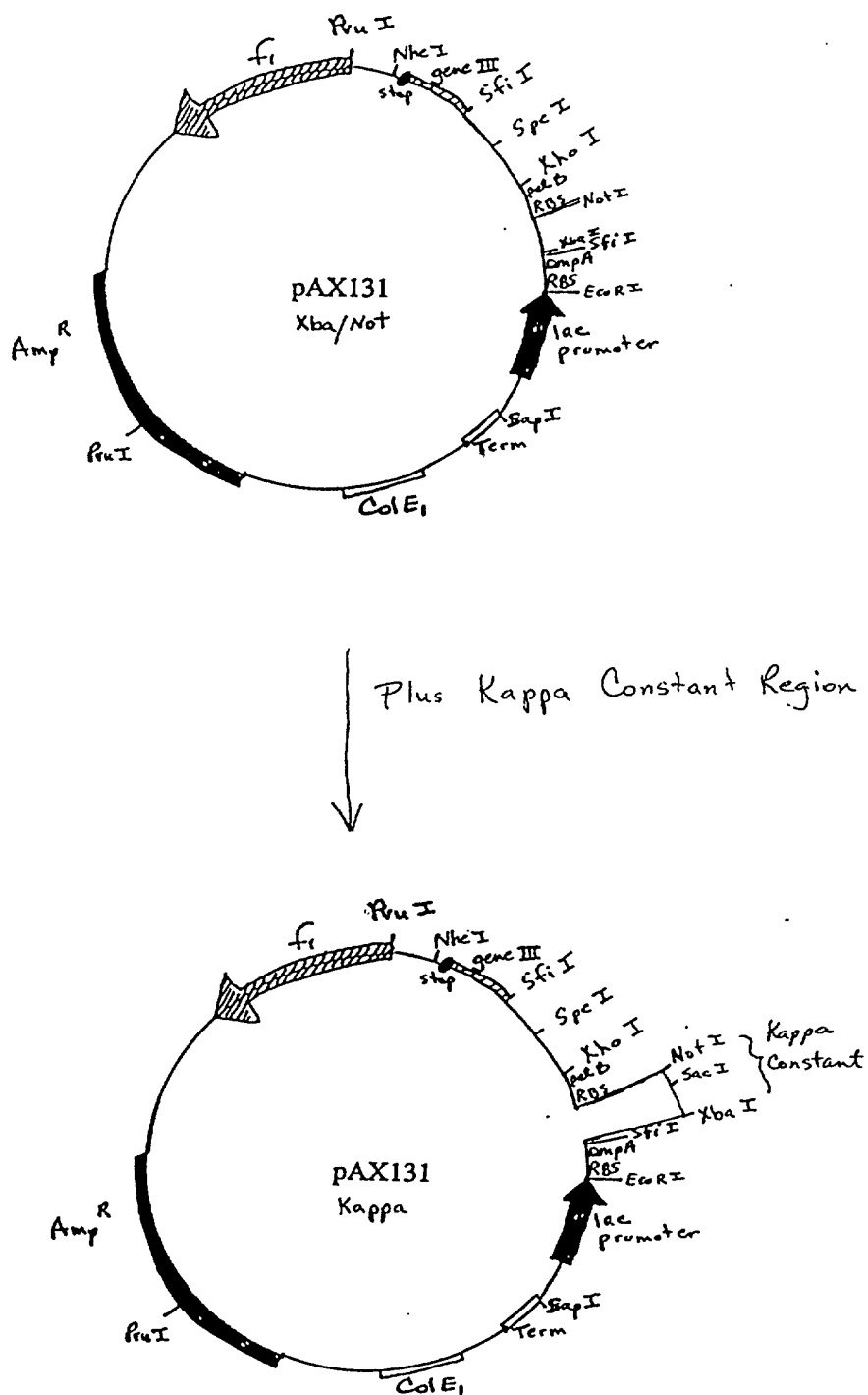


Fig. 18

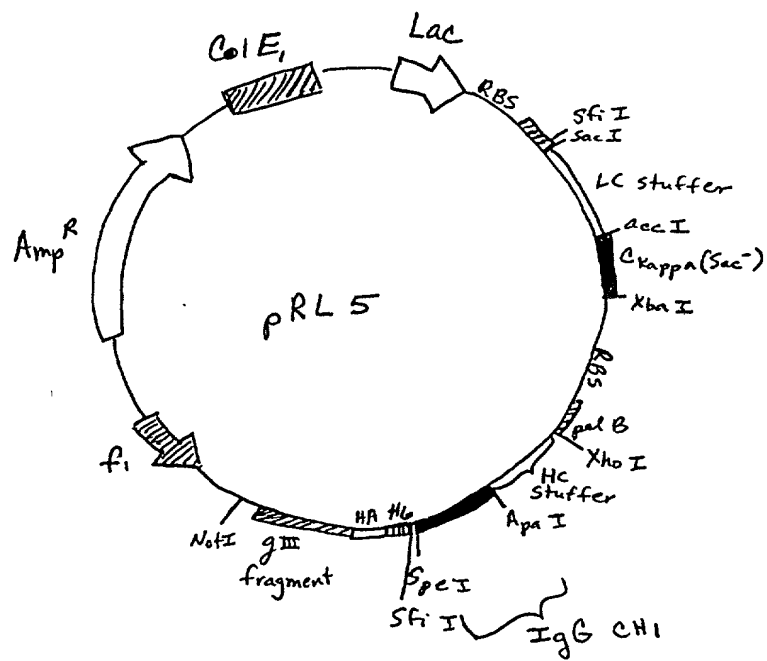


Fig. 19

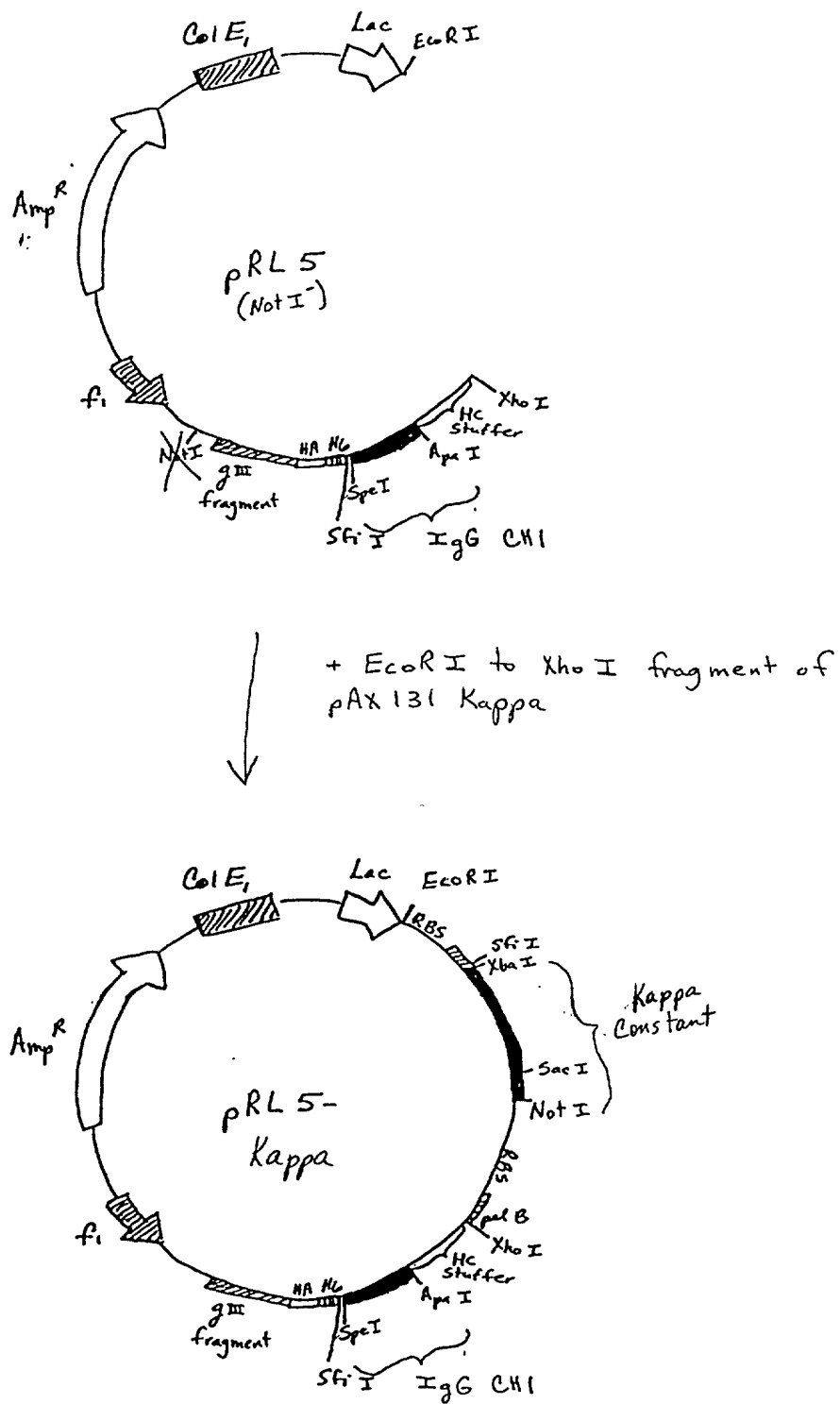


Fig. 20



AACATTCCGTGCGCCCTTATTCCCTTTTTCGGCATTTTTCCTCCCTGTTTTTGCCTCACCAGAAACGCTGGTGAAGTAAAGATGCTGAAGATCA 700

beta-lactamase

ApalI
BssSI
Eco57I

AclI
XmnI

GTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTTTTTCGCCCCGGAAGAACGTTTTTCCAATGATGAGCACTTTT 800

beta-lactamase

BcgI

BcgI
ScaI

AAAGTTCTGCTATGTGGCGCGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACT 900

beta-lactamase

BtsI

BtsI

CACCAGTCACAGAAAAGCATCTACGGATGGCATGACAGTAAGAGAATTATGCAGTGTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCT 1000

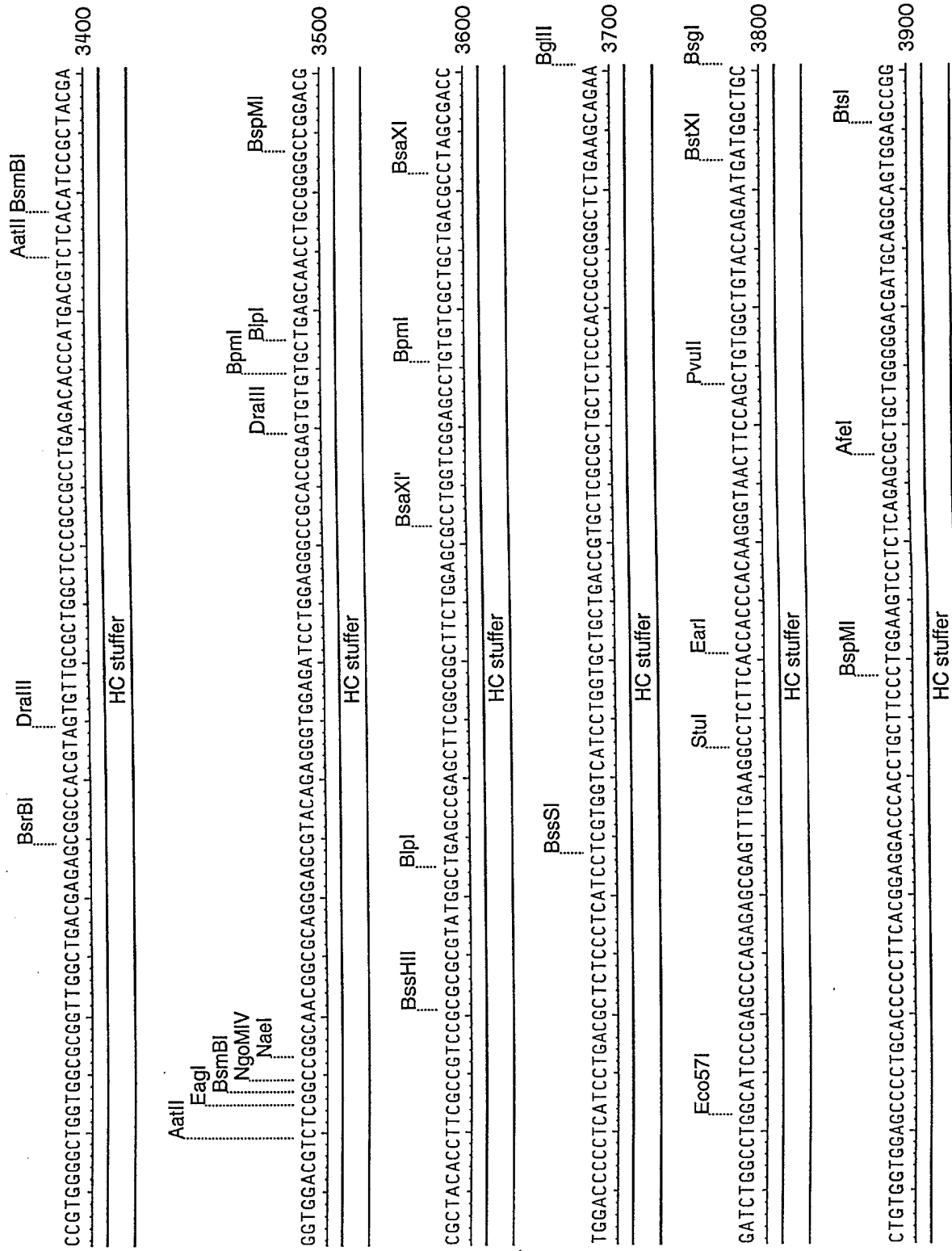
beta-lactamase

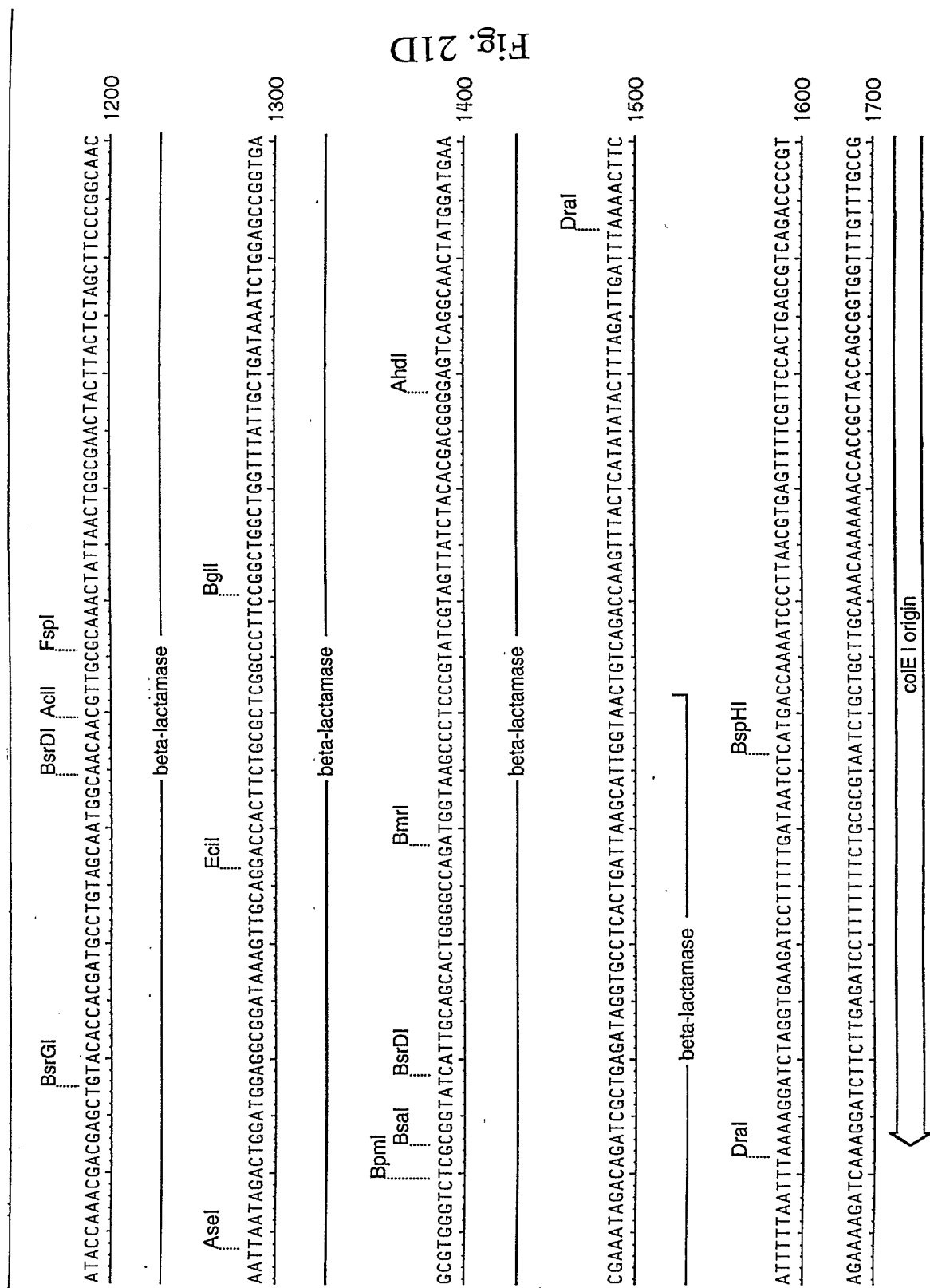
PvuI

GACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACGGAGCTGAATGAAGCC 1100

beta-lactamase

Fig. 21B





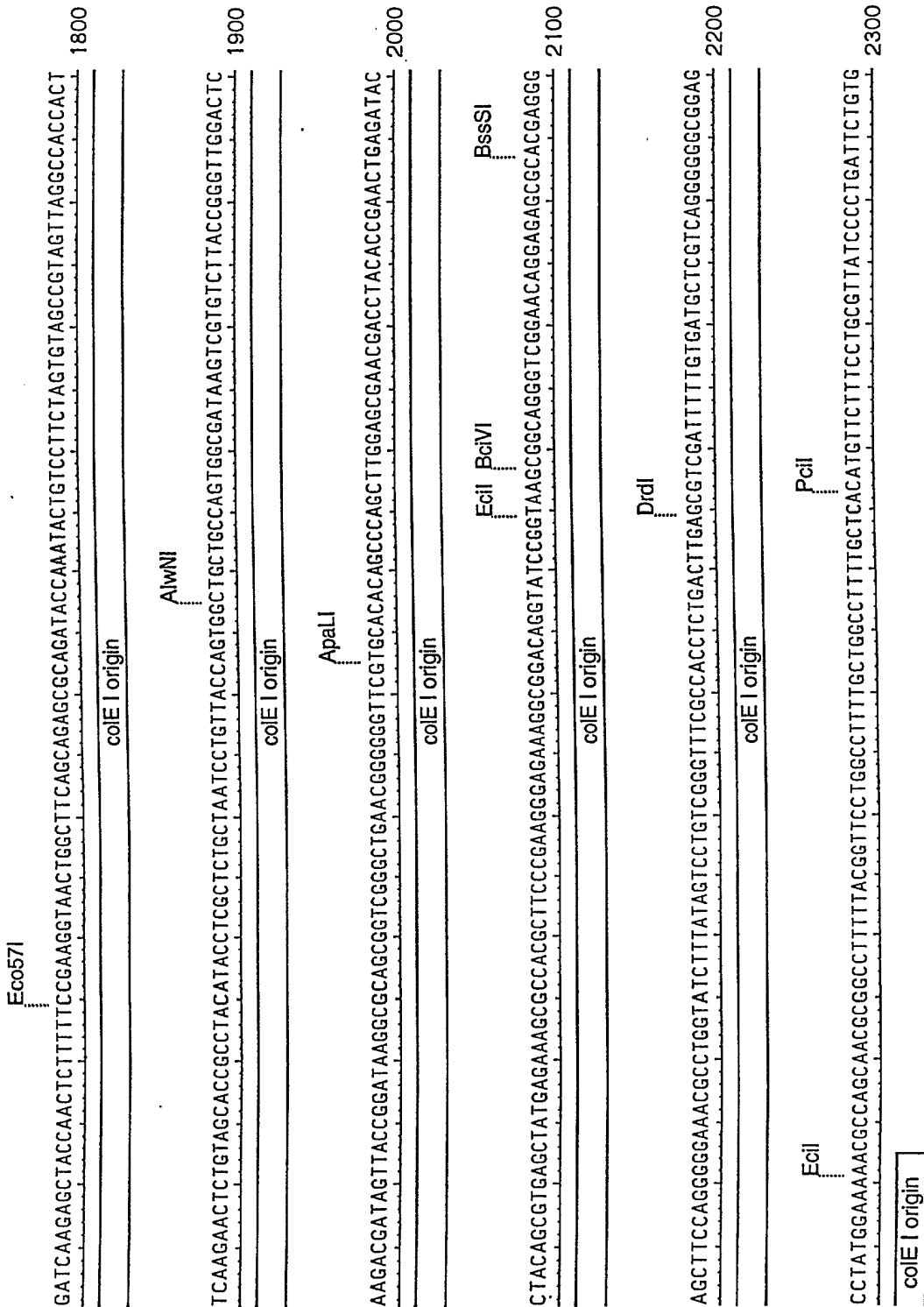


Fig. 21E

Fig. 21F

GGAAGGTGGATAACGCCCTCCAATCGGGTAACGCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCT 2900

BbvCI Bpu10I BlnI

Kappa constant

CAGCAAACACAGACTACGACAAACACAAAGTCTACGGCTGCCAAGTCACCCATCAGGGCCGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 3000

AlwNI Bpu10I EcoRI SacI

Kappa constant

TAAGCGGCGCAC TAGATATAATTAGGAGATAAATATGAAATATCTGCTGCCGACCGCGGCGGGCCCTGCTGCTGCTGCGCGCGCAGCCGGCGATGG 3100

EagI NotI SacI NgoMIV NaeI

optimized pel B leader

rb

CGCTCGAGCTGATGAGCCATGGAAGCTGTGCGCCTGCACCAAGCTCCACAGGCTCGTGGTGGGTGCGCTTCTGGTGTTCGCTGCCTACAGCCGACACG 3200

XhoI NcoI BspI BssSI BclI BlnI

HC stuffer

TCGAGCTTCGTGCCCCCTAGAGTTGCGCGTTCACAGCAGCCCTCCGGCGCTCCGGGATATCACCGTGTATCCACATCAATGAAGTAGTGTCTCTAGAGCCCC 3300

BclI EcoRV

HC stuffer

Fig. 21G

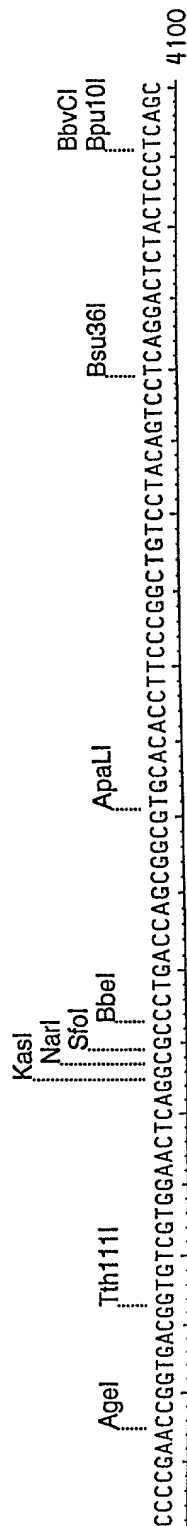
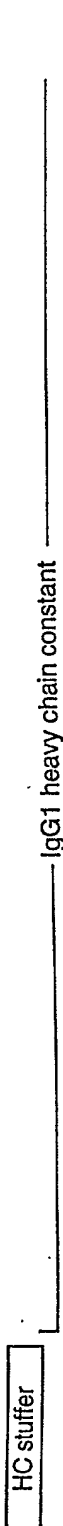
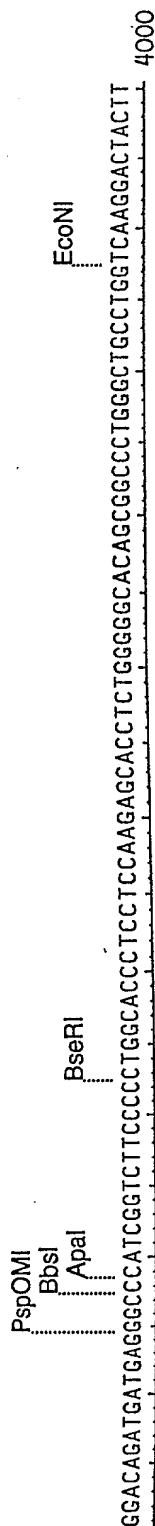


Fig. 21H

